

SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: Bryan, Bruce
- (ii) TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Heller Ehrman White & McAuliffe
 - (B) STREET: 4250 Executive Square, 7th Floor
 - (C) CITY: La Jolla
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 09/444,762
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 09/444,762
 - (B) FILING DATE: 11-22-99
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/757,046
 - (B) FILING DATE: 11-25-96
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/597,274
 - (B) FILING DATE: 02-06-96
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Seidman, Stephanie L
 - (B) REGISTRATION NUMBER: 33,779
 - (C) REFERENCE/DOCKET NUMBER: 24727-105F
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 619-450-8400
 - (B) TELEFAX: 619-450-8499
 - (C) TELEX:
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...942
 (D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGC	TTA	AAG	ATG	ACT	TCG	AAA	GTT	TAT	GAT	CCA	GAA	CAA	AGG	AAA	CGG	48
Ser	Leu	Lys	Met	Thr	Ser	Lys	Val	Tyr	Asp	Pro	Glu	Gln	Arg	Lys	Arg	
1				5				10						15		
ATG	ATA	ACT	GGT	CCG	CAG	TGG	TGG	GCC	AGA	TGT	AAA	CAA	ATG	AAT	GTT	96
Met	Ile	Thr	Gly	Pro	Gln	Trp	Trp	Ala	Arg	Cys	Lys	Gln	Met	Asn	Val	
			20					25					30			
CTT	GAT	TCA	TTT	ATT	AAT	TAT	TAT	GAT	TCA	GAA	AAA	CAT	GCA	GAA	AAT	144
Leu	Asp	Ser	Phe	Ile	Asn	Tyr	Tyr	Asp	Ser	Glu	Lys	His	Ala	Glu	Asn	
		35				40						45				
GCT	GTT	ATT	TTT	TTA	CAT	GGT	AAC	GCG	GCC	TCT	TCT	TAT	TTA	TGG	CGA	192
Ala	Val	Ile	Phe	Leu	His	Gly	Asn	Ala	Ala	Ser	Ser	Tyr	Leu	Trp	Arg	
	50					55				60						
CAT	GTT	GTG	CCA	CAT	ATT	GAG	CCA	GTA	GCG	CGG	TGT	ATT	ATA	CCA	GAT	240
His	Val	Val	Pro	His	Ile	Glu	Pro	Val	Ala	Arg	Cys	Ile	Ile	Pro	Asp	
65					70					75				80		
CTT	ATT	GGT	ATG	GGC	AAA	TCA	GGC	AAA	TCT	GGT	AAT	GGT	TCT	TAT	AGG	288
Leu	Ile	Gly	Met	Gly	Lys	Ser	Gly	Lys	Ser	Gly	Asn	Gly	Ser	Tyr	Arg	
				85					90					95		
TTA	CTT	GAT	CAT	TAC	AAA	TAT	CTT	ACT	GCA	TGG	TTG	AAC	TTC	TTA	ATT	336
Leu	Leu	Asp	His	Tyr	Lys	Tyr	Leu	Thr	Ala	Trp	Leu	Asn	Phe	Leu	Ile	
			100					105					110			
TAC	CAA	AGA	AGA	TCA	TTT	TTT	GTC	GGC	CAT	GAT	TGG	GGT	GCT	TGT	TTG	384
Tyr	Gln	Arg	Arg	Ser	Phe	Phe	Val	Gly	His	Asp	Trp	Gly	Ala	Cys	Leu	
		115					120					125				
GCA	TTT	CAT	TAT	AGC	TAT	GAG	CAT	CAA	GAT	AAG	ATC	AAA	GCA	ATA	GTT	432
Ala	Phe	His	Tyr	Ser	Tyr	Glu	His	Gln	Asp	Lys	Ile	Lys	Ala	Ile	Val	
	130					135					140					
CAC	GCT	GAA	AGT	GTA	GTA	GAT	GTG	ATT	GAA	TCA	TGG	GAT	GAA	TGG	CCT	480
His	Ala	Glu	Ser	Val	Val	Asp	Val	Ile	Glu	Ser	Trp	Asp	Glu	Trp	Pro	
145					150					155					160	
GAT	ATT	GAA	GAA	GAT	ATT	GCG	TTG	ATC	AAA	TCT	GAA	GAA	GGA	GAA	AAA	528
Asp	Ile	Glu	Glu	Asp	Ile	Ala	Leu	Ile	Lys	Ser	Glu	Glu	Gly	Glu	Lys	
				165					170					175		
ATG	GTT	TTG	GAG	AAT	AAC	TTC	TTC	GTG	GAA	ACC	ATG	TTG	CCA	TCA	AAA	576
Met	Val	Leu	Glu	Asn	Asn	Phe	Phe	Val	Glu	Thr	Met	Leu	Pro	Ser	Lys	
			180					185					190			
ATC	ATG	AGA	AAG	TTA	GAA	CCA	GAA	GAA	TTT	GCA	GCA	TAT	CTT	GAA	CCA	624
Ile	Met	Arg	Lys	Leu	Glu	Pro	Glu	Glu	Phe	Ala	Ala	Tyr	Leu	Glu	Pro	
		195					200					205				
TTC	AAA	GAG	AAA	GGT	GAA	GTT	CGT	CGT	CCA	ACA	TTA	TCA	TGG	CCT	CGT	672

Phe	Lys	Glu	Lys	Gly	Glu	Val	Arg	Arg	Pro	Thr	Leu	Ser	Trp	Pro	Arg		
210						215					220						
GAA	ATC	CCG	TTA	GTA	AAA	GGT	GGT	AAA	CCT	GAC	GTT	GTA	CAA	ATT	GTT		720
Glu	Ile	Pro	Leu	Val	Lys	Gly	Gly	Lys	Pro	Asp	Val	Val	Gln	Ile	Val		
225					230					235					240		
AGG	AAT	TAT	AAT	GCT	TAT	CTA	CGT	GCA	AGT	GAT	GAT	TTA	CCA	AAA	ATG		768
Arg	Asn	Tyr	Asn	Ala	Tyr	Leu	Arg	Ala	Ser	Asp	Asp	Leu	Pro	Lys	Met		
				245					250					255			
TTT	ATT	GAA	TCG	GAT	CCA	GGA	TTC	TTT	TCC	AAT	GCT	ATT	GTT	GAA	GGC		816
Phe	Ile	Glu	Ser	Asp	Pro	Gly	Phe	Phe	Ser	Asn	Ala	Ile	Val	Glu	Gly		
				260				265					270				
GCC	AAG	AAG	TTT	CCT	AAT	ACT	GAA	TTT	GTC	AAA	GTA	AAA	GGT	CTT	CAT		864
Ala	Lys	Lys	Phe	Pro	Asn	Thr	Glu	Phe	Val	Lys	Val	Lys	Gly	Leu	His		
		275					280					285					
TTT	TCG	CAA	GAA	GAT	GCA	CCT	GAT	GAA	ATG	GGA	AAA	TAT	ATC	AAA	TCG		912
Phe	Ser	Gln	Glu	Asp	Ala	Pro	Asp	Glu	Met	Gly	Lys	Tyr	Ile	Lys	Ser		
	290					295					300						
TTC	GTT	GAG	CGA	GTT	CTC	AAA	AAT	GAA	CAA	TAA	TTACTTTGGT	TTTTTATTTA					965
Phe	Val	Glu	Arg	Val	Leu	Lys	Asn	Glu	Gln								
305					310												
CATTTTTC	CCG	GGT	TTA	ATA	ATG	TATTTTCA	CAAC	AATTTTAT	TTT	TA	ACTGA	ATA					1025
TTTCACAG	GGG	AAC	ATTC	CATA	TATGTTG	ATT	AATTTAG	CTC	GA	ACTTTACT	CTGTC	CATATC					1085
ATTTTGG	AAT	ATTACCT	CTT	TCAATG	AAAC	TTTATAA	ACA	GTGGTTCA	AT	TAATTA	ATAT						1145
ATATTATA	AT	TACATTT	GT	ATGTA	ATAA	CTCGGTT	TTA	TTATAA	AAAAA	A							1196

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1665
- (D) OTHER INFORMATION: Cypridina hilgendorffii luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: EP 0 387 355 TORAY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG	AAG	CTA	ATA	ATT	CTG	TCT	ATT	ATA	TTG	GCC	TAC	TGT	GTC	ACA	GTC		48
Met	Lys	Leu	Ile	Ile	Leu	Ser	Ile	Ile	Leu	Ala	Tyr	Cys	Val	Thr	Val		
1				5					10					15			
AAC	TGC	CAG	GAT	GCA	TGT	CCT	GTA	GAA	GCT	GAA	GCA	CCG	TCA	AGT	ACA		96
Asn	Cys	Gln	Asp	Ala	Cys	Pro	Val	Glu	Ala	Glu	Ala	Pro	Ser	Ser	Thr		
			20					25					30				
CCA	ACA	GTC	CCA	ACA	TCT	TGT	GAA	GCT	AAA	GAA	GGA	GAA	TGT	ATC	GAT		144
Pro	Thr	Val	Pro	Thr	Ser	Cys	Glu	Ala	Lys	Glu	Gly	Glu	Cys	Ile	Asp		
		35					40					45					

ACC	AGA	TGC	GCA	ACA	TGT	AAA	CGA	GAC	ATA	CTA	TCA	GAC	GGA	CTG	TGT	192
Thr	Arg	Cys	Ala	Thr	Cys	Lys	Arg	Asp	Ile	Leu	Ser	Asp	Gly	Leu	Cys	
	50					55					60					
GAA	AAT	AAA	CCA	GGG	AAG	ACA	TGC	TGT	AGA	ATG	TGC	CAG	TAT	GTA	ATT	240
Glu	Asn	Lys	Pro	Gly	Lys	Thr	Cys	Cys	Arg	Met	Cys	Gln	Tyr	Val	Ile	
65					70					75					80	
GAA	TCC	AGA	GTA	GAA	GCT	GCT	GGA	TAT	TTT	AGA	ACG	TTT	TAC	GCC	AAA	288
Glu	Ser	Arg	Val	Glu	Ala	Ala	Gly	Tyr	Phe	Arg	Thr	Phe	Tyr	Ala	Lys	
				85					90					95		
AGA	TTT	AAT	TTT	CAG	GAA	CCT	GGT	AAA	TAT	GTG	CTG	GCT	CGA	GGA	ACC	336
Arg	Phe	Asn	Phe	Gln	Glu	Pro	Gly	Lys	Tyr	Val	Leu	Ala	Arg	Gly	Thr	
			100					105					110			
AAG	GGT	GGC	GAC	TGG	TCT	GTA	ACC	CTC	ACC	ATG	GAG	AAT	CTA	GAT	GGA	384
Lys	Gly	Gly	Asp	Trp	Ser	Val	Thr	Leu	Thr	Met	Glu	Asn	Leu	Asp	Gly	
		115					120					125				
CAG	AAG	GGA	GCT	GTA	CTG	ACT	AAG	ACA	ACA	CTG	GAG	GTA	GTA	GGA	GAC	432
Gln	Lys	Gly	Ala	Val	Leu	Thr	Lys	Thr	Thr	Leu	Glu	Val	Val	Gly	Asp	
	130					135					140					
GTA	ATA	GAC	ATT	ACT	CAA	GCT	ACT	GCA	GAT	CCT	ATC	ACA	GTT	AAC	GGA	480
Val	Ile	Asp	Ile	Thr	Gln	Ala	Thr	Ala	Asp	Pro	Ile	Thr	Val	Asn	Gly	
145					150					155					160	
GGA	GCT	GAC	CCA	GTT	ATC	GCT	AAC	CCG	TTC	ACA	ATT	GGT	GAG	GTG	ACC	528
Gly	Ala	Asp	Pro	Val	Ile	Ala	Asn	Pro	Phe	Thr	Ile	Gly	Glu	Val	Thr	
				165				170						175		
ATT	GCT	GTT	GTC	GAA	ATA	CCC	GGC	TTC	AAT	ATT	ACA	GTC	ATC	GAA	TTC	576
Ile	Ala	Val	Val	Glu	Ile	Pro	Gly	Phe	Asn	Ile	Thr	Val	Ile	Glu	Phe	
			180					185					190			
TTT	AAA	CTA	ATC	GTG	ATA	GAT	ATT	CTG	GGA	GGA	AGA	TCT	GTG	AGA	ATT	624
Phe	Lys	Leu	Ile	Val	Ile	Asp	Ile	Leu	Gly	Gly	Arg	Ser	Val	Arg	Ile	
		195					200					205				
GCT	CCA	GAC	ACA	GCA	AAC	AAA	GGA	CTG	ATA	TCT	GGT	ATC	TGT	GGT	AAT	672
Ala	Pro	Asp	Thr	Ala	Asn	Lys	Gly	Leu	Ile	Ser	Gly	Ile	Cys	Gly	Asn	
	210					215					220					
CTG	GAG	ATG	AAT	GAC	GCT	GAT	GAC	TTT	ACT	ACA	GAC	GCA	GAT	CAG	CTG	720
Leu	Glu	Met	Asn	Asp	Ala	Asp	Asp	Phe	Thr	Thr	Asp	Ala	Asp	Gln	Leu	
225					230					235				240		
GCG	ATC	CAA	CCC	AAC	ATA	AAC	AAA	GAG	TTC	GAC	GGC	TGC	CCA	TTC	TAC	768
Ala	Ile	Gln	Pro	Asn	Ile	Asn	Lys	Glu	Phe	Asp	Gly	Cys	Pro	Phe	Tyr	
				245					250					255		
GGG	AAT	CCT	TCT	GAT	ATC	GAA	TAC	TGC	AAA	GGT	CTC	ATG	GAG	CCA	TAC	816
Gly	Asn	Pro	Ser	Asp	Ile	Glu	Tyr	Cys	Lys	Gly	Leu	Met	Glu	Pro	Tyr	
			260					265				270				
AGA	GCT	GTA	TGT	CGT	AAC	AAT	ATC	AAC	TTC	TAC	TAT	TAC	ACT	CTG	TCC	864
Arg	Ala	Val	Cys	Arg	Asn	Asn	Ile	Asn	Phe	Tyr	Tyr	Tyr	Thr	Leu	Ser	
		275					280					285				
TGC	GCC	TTC	GCT	TAC	TGT	ATG	GGA	GGA	GAA	GAA	AGA	GCT	AAA	CAC	GTC	912
Cys	Ala	Phe	Ala	Tyr	Cys	Met	Gly	Gly	Glu	Glu	Arg	Ala	Lys	His	Val	
	290					295					300					
CTT	TTC	GAC	TAT	GTT	GAG	ACA	TGC	GCT	GCA	CCG	GAA	ACG	AGA	GGA	ACG	960

Leu 305	Phe	Asp	Tyr	Val	Glu 310	Thr	Cys	Ala	Ala	Pro 315	Glu	Thr	Arg	Gly	Thr 320	
TGT Cys	GTT Val	TTA Leu	TCA Ser	GGA Gly	CAT His	ACT Thr	TTC Phe	TAT Tyr	GAC Asp	ACA Thr	TTC Phe	GAC Asp	AAA Lys	GCC Ala	AGA Arg	1008
TAT Tyr	CAA Gln	TTT Phe	CAG Gln	GGC Gly	CCA Pro	TGC Cys	AAA Lys	GAG Glu	CTT Leu	CTG Leu	ATG Met	GCC Ala	GCA Ala	GAC Asp	TGT Cys	1056
TAC Tyr	TGG Trp	AAC Asn	ACA Thr	TGG Trp	GAT Asp	GTA Val	AAG Lys	GTT Val	TCA Ser	CAT His	AGA Arg	GAT Asp	GTT Val	GAG Glu	TCA Ser	1104
TAC Tyr	ACT Thr	GAG Glu	GTA Val	GAG Glu	AAA Lys	GTA Val	ACA Thr	ATC Ile	AGG Arg	AAA Lys	CAG Gln	TCA Ser	ACT Thr	GTA Val	GTA Val	1152
GAT Asp	TTG Leu	ATT Ile	GTG Val	GAT Asp	GGC Gly	AAG Lys	CAG Gln	GTC Val	AAG Lys	GTT Val	GGA Gly	GGA Gly	GTG Val	GAT Asp	GTA Val	1200
TCT Ser	ATC Ile	CCG Pro	TAC Tyr	AGT Ser	TCT Ser	GAG Glu	AAC Asn	ACA Thr	TCC Ser	ATA Ile	TAC Tyr	TGG Trp	CAG Gln	GAT Asp	GGA Gly	1248
GAC Asp	ATC Ile	CTG Leu	ACG Thr	ACG Thr	GCC Ala	ATC Ile	CTA Leu	CCT Pro	GAA Glu	GCT Ala	CTT Leu	GTC Val	GTT Val	AAG Lys	TTC Phe	1296
AAC Asn	TTT Phe	AAG Lys	CAG Gln	CTC Leu	CTT Leu	GTA Val	GTT Val	CAT His	ATC Ile	AGA Arg	GAT Asp	CCA Pro	TTC Phe	GAT Asp	GGA Gly	1344
AAG Lys	ACA Thr	TGC Cys	GGC Gly	ATA Ile	TGT Cys	GGT Gly	AAC Asn	TAT Tyr	AAT Asn	CAA Gln	GAT Asp	TCA Ser	ACT Thr	GAT Asp	GAT Asp	1392
TTC Phe	TTT Phe	GAC Asp	GCA Ala	GAA Glu	GGA Gly	GCA Ala	TGC Cys	GCT Ala	CTG Leu	ACC Thr	CCC Pro	AAT Asn	CCC Pro	CCA Pro	GGA Gly	1440
TGT Cys	ACA Thr	GAG Glu	GAG Glu	CAG Gln	AAA Lys	CCA Pro	GAA Glu	GCT Ala	GAG Glu	CGA Arg	CTC Leu	TGC Cys	AAT Asn	AGT Ser	CTA Leu	1488
TTT Phe	GAT Asp	AGT Ser	TCT Ser	ATC Ile	GAC Asp	GAG Glu	AAA Lys	TGT Cys	AAT Asn	GTC Val	TGC Cys	TAC Tyr	AAG Lys	CCT Pro	GAC Asp	1536
CGT Arg	ATT Ile	GCA Ala	CGA Arg	TGT Cys	ATG Met	TAC Tyr	GAG Glu	TAT Tyr	TGC Cys	CTG Leu	AGG Arg	GGA Gly	CAG Gln	CAA Gln	GGA Gly	1584
TTC Phe	TGT Cys	GAC Asp	CAT His	GCT Ala	TGG Trp	GAG Glu	TTC Phe	AAA Lys	AAA Lys	GAA Glu	TGC Cys	TAC Tyr	ATA Ile	AAG Lys	CAT His	1632
GGA Gly	GAC Asp	ACT Thr	CTA Leu	GAA Glu	GTA Val	CCA Pro	CCT Pro	GAA Glu	TGC Cys	CAA Gln	TAA	ATGAACAAAG				1678
ATACAGAAGC	TAAGACTACT	ACAGCAGAAG	ATAAAAGAGA	AGCTGTAGTT	CTTCAAAAAC											1738
AGTATATTTT	GATGTACTCA	TTGTTTACTT	ACATAAAAAT	AAATTGTTAT	TATCATAACG											1798

TAAAGAAAAA AAAAAAAAAA AAAA

1822

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1644
- (D) OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)

(x) PUBLICATION INFORMATION:

PATENT NO.: 4,968,613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG	GAA	AAC	ATG	GAA	AAC	GAT	GAA	AAT	ATT	GTA	GTT	GGA	CCT	AAA	CCG	48
Met	Glu	Asn	Met	Glu	Asn	Asp	Glu	Asn	Ile	Val	Val	Gly	Pro	Lys	Pro	
1				5					10					15		
TTT	TAC	CCT	ATC	GAA	GAG	GGA	TCT	GCT	GGA	ACA	CAA	TTA	CGC	AAA	TAC	96
Phe	Tyr	Pro	Ile	Glu	Glu	Gly	Ser	Ala	Gly	Thr	Gln	Leu	Arg	Lys	Tyr	
			20					25					30			
ATG	GAG	CGA	TAT	GCA	AAA	CTT	GGC	GCA	ATT	GCT	TTT	ACA	AAT	GCA	GTT	144
Met	Glu	Arg	Tyr	Ala	Lys	Leu	Gly	Ala	Ile	Ala	Phe	Thr	Asn	Ala	Val	
			35				40					45				
ACT	GGT	GTT	GAT	TAT	TCT	TAC	GCC	GAA	TAC	TTG	GAG	AAA	TCA	TGT	TGT	192
Thr	Gly	Val	Asp	Tyr	Ser	Tyr	Ala	Glu	Tyr	Leu	Glu	Lys	Ser	Cys	Cys	
	50					55					60					
CTA	GGA	AAA	GCT	TTG	CAA	AAT	TAT	GGT	TTG	GTT	GTT	GAT	GGC	AGA	ATT	240
Leu	Gly	Lys	Ala	Leu	Gln	Asn	Tyr	Gly	Leu	Val	Val	Asp	Gly	Arg	Ile	
65					70				75					80		
GCG	TTA	TGC	AGT	GAA	AAC	TGT	GAA	GAA	TTT	TTT	ATT	CCT	GTA	ATA	GCC	288
Ala	Leu	Cys	Ser	Glu	Asn	Cys	Glu	Glu	Phe	Phe	Ile	Pro	Val	Ile	Ala	
			85						90					95		
GGA	CTG	TTT	ATA	GGT	GTA	GGT	GTT	GCA	CCC	ACT	AAT	GAG	ATT	TAC	ACT	336
Gly	Leu	Phe	Ile	Gly	Val	Gly	Val	Ala	Pro	Thr	Asn	Glu	Ile	Tyr	Thr	
			100					105					110			
TTA	CGT	GAA	CTG	GTT	CAC	AGT	TTA	GGT	ATC	TCT	AAA	CCA	ACA	ATT	GTA	384
Leu	Arg	Glu	Leu	Val	His	Ser	Leu	Gly	Ile	Ser	Lys	Pro	Thr	Ile	Val	
			115				120					125				
TTT	AGT	TCT	AAA	AAA	GGC	TTA	GAT	AAA	GTT	ATA	ACA	GTA	CAG	AAA	ACA	432
Phe	Ser	Ser	Lys	Lys	Gly	Leu	Asp	Lys	Val	Ile	Thr	Val	Gln	Lys	Thr	
	130					135				140						
GTA	ACT	ACT	ATT	AAA	ACC	ATT	GTT	ATA	CTA	GAT	AGC	AAA	GTT	GAT	TAT	480
Val	Thr	Thr	Ile	Lys	Thr	Ile	Val	Ile	Leu	Asp	Ser	Lys	Val	Asp	Tyr	
145					150				155					160		
CGA	GGA	TAT	CAA	TGT	CTG	GAC	ACC	TTT	ATA	AAA	AGA	AAC	ACT	CCA	CCA	528

Arg	Gly	Tyr	Gln	Cys 165	Leu	Asp	Thr	Phe	Ile 170	Lys	Arg	Asn	Thr	Pro 175	Pro		
GGT	TTT	CAA	GCA	TCC	AGT	TTC	AAA	ACT	GTG	GAA	GTT	GAC	CGT	AAA	GAA		576
Gly	Phe	Gln	Ala	Ser	Ser	Phe	Lys	Thr	Val	Glu	Val	Asp	Arg	Lys	Glu		
			180					185					190				
CAA	GTT	GCT	CTT	ATA	ATG	AAC	TCT	TCG	GGT	TCT	ACC	GGT	TTG	CCA	AAA		624
Gln	Val	Ala	Leu	Ile	Met	Asn	Ser	Ser	Gly	Ser	Thr	Gly	Leu	Pro	Lys		
		195					200					205					
GGC	GTA	CAA	CTT	ACT	CAC	GAA	AAT	ACA	GTC	ACT	AGA	TTT	TCT	CAT	GCT		672
Gly	Val	Gln	Leu	Thr	His	Glu	Asn	Thr	Val	Thr	Arg	Phe	Ser	His	Ala		
	210					215					220						
AGA	GAT	CCG	ATT	TAT	GGT	AAC	CAA	GTT	TCA	CCA	GGC	ACC	GCT	GTT	TTA		720
Arg	Asp	Pro	Ile	Tyr	Gly	Asn	Gln	Val	Ser	Pro	Gly	Thr	Ala	Val	Leu		
225					230					235					240		
ACT	GTC	GTT	CCA	TTC	CAT	CAT	GGT	TTT	GGT	ATG	TTC	ACT	ACT	CTA	GGG		768
Thr	Val	Val	Pro	Phe	His	His	Gly	Phe	Gly	Met	Phe	Thr	Thr	Leu	Gly		
				245					250					255			
TAT	TTA	ATT	TGT	GGT	TTT	CGT	GTT	GTA	ATG	TTA	ACA	AAA	TTC	GAT	GAA		816
Tyr	Leu	Ile	Cys	Gly	Phe	Arg	Val	Val	Met	Leu	Thr	Lys	Phe	Asp	Glu		
			260					265					270				
GAA	ACA	TTT	TTA	AAA	ACT	CTA	CAA	GAT	TAT	AAA	TGT	ACA	AGT	GTT	ATT		864
Glu	Thr	Phe	Leu	Lys	Thr	Leu	Gln	Asp	Tyr	Lys	Cys	Thr	Ser	Val	Ile		
		275					280					285					
CTT	GTA	CCG	ACC	TTG	TTT	GCA	ATT	CTC	AAC	AAA	AGT	GAA	TTA	CTC	AAT		912
Leu	Val	Pro	Thr	Leu	Phe	Ala	Ile	Leu	Asn	Lys	Ser	Glu	Leu	Leu	Asn		
	290					295					300						
AAA	TAC	GAT	TTG	TCA	AAT	TTA	GTT	GAG	ATT	GCA	TCT	GGC	GGA	GCA	CCT		960
Lys	Tyr	Asp	Leu	Ser	Asn	Leu	Val	Glu	Ile	Ala	Ser	Gly	Gly	Ala	Pro		
305					310					315					320		
TTA	TCA	AAA	GAA	GTT	GGT	GAA	GCT	GTT	GCT	AGA	CGC	TTT	AAT	CTT	CCC		1008
Leu	Ser	Lys	Glu	Val	Gly	Glu	Ala	Val	Ala	Arg	Arg	Phe	Asn	Leu	Pro		
				325					330					335			
GGT	GTT	CGT	CAA	GGT	TAT	GGT	TTA	ACA	GAA	ACA	ACA	TCT	GCC	ATT	ATT		1056
Gly	Val	Arg	Gln	Gly	Tyr	Gly	Leu	Thr	Glu	Thr	Thr	Ser	Ala	Ile	Ile		
			340					345					350				
ATT	ACA	CCA	GAA	GGA	GAC	GAT	AAA	CCA	GGA	GCT	TCT	GGA	AAA	GTC	GTG		1104
Ile	Thr	Pro	Glu	Gly	Asp	Asp	Lys	Pro	Gly	Ala	Ser	Gly	Lys	Val	Val		
		355					360					365					
CCG	TTG	TTT	AAA	GCA	AAA	GTT	ATT	GAT	CTT	GAT	ACC	AAA	AAA	TCT	TTA		1152
Pro	Leu	Phe	Lys	Ala	Lys	Val	Ile	Asp	Leu	Asp	Thr	Lys	Lys	Ser	Leu		
	370					375					380						
GGT	CCT	AAC	AGA	CGT	GGA	GAA	GTT	TGT	GTT	AAA	GGA	CCT	ATG	CTT	ATG		1200
Gly	Pro	Asn	Arg	Arg	Gly	Glu	Val	Cys	Val	Lys	Gly	Pro	Met	Leu	Met		
385					390					395				400			
AAA	GGT	TAT	GTA	AAT	AAT	CCA	GAA	GCA	ACA	AAA	GAA	CTT	ATT	GAC	GAA		1248
Lys	Gly	Tyr	Val	Asn	Asn	Pro	Glu	Ala	Thr	Lys	Glu	Leu	Ile	Asp	Glu		
				405					410					415			
GAA	GGT	TGG	CTG	CAC	ACC	GGA	GAT	ATT	GGA	TAT	TAT	GAT	GAA	GAA	AAA		1296
Glu	Gly	Trp	Leu	His	Thr	Gly	Asp	Ile	Gly	Tyr	Tyr	Asp	Glu	Glu	Lys		

420										425					430					
CAT	TTC	TTT	ATT	GTC	GAT	CGT	TTG	AAG	TCT	TTA	ATC	AAA	TAC	AAA	GGA	1344				
His	Phe	Phe	Ile	Val	Asp	Arg	Leu	Lys	Ser	Leu	Ile	Lys	Tyr	Lys	Gly					
		435					440					445								
TAC	CAA	GTA	CCA	CCT	GCC	GAA	TTA	GAA	TCC	GTT	CTT	TTG	CAA	CAT	CCA	1392				
Tyr	Gln	Val	Pro	Pro	Ala	Glu	Leu	Glu	Ser	Val	Leu	Leu	Gln	His	Pro					
	450					455					460									
TCT	ATC	TTT	GAT	GCT	GGT	GTT	GCC	GGC	GTT	CCT	GAT	CCT	GTA	GCT	GGC	1440				
Ser	Ile	Phe	Asp	Ala	Gly	Val	Ala	Gly	Val	Pro	Asp	Pro	Val	Ala	Gly					
465					470					475					480					
GAG	CTT	CCA	GGA	GCC	GTT	GTT	GTA	CTG	GAA	AGC	GGA	AAA	AAT	ATG	ACC	1488				
Glu	Leu	Pro	Gly	Ala	Val	Val	Val	Leu	Glu	Ser	Gly	Lys	Asn	Met	Thr					
			485						490					495						
GAA	AAA	GAA	GTA	ATG	GAT	TAT	GTT	GCA	AGT	CAA	GTT	TCA	AAT	GCA	AAA	1536				
Glu	Lys	Glu	Val	Met	Asp	Tyr	Val	Ala	Ser	Gln	Val	Ser	Asn	Ala	Lys					
			500					505					510							
CGT	TTA	CGT	GGT	GGT	GTT	CGT	TTT	GTG	GAT	GAA	GTA	CCT	AAA	GGT	CTT	1584				
Arg	Leu	Arg	Gly	Gly	Val	Arg	Phe	Val	Asp	Glu	Val	Pro	Lys	Gly	Leu					
		515					520					525								
ACT	GGA	AAA	ATT	GAC	GGC	AGA	GCA	ATT	AGA	GAA	ATC	CTT	AAG	AAA	CCA	1632				
Thr	Gly	Lys	Ile	Asp	Gly	Arg	Ala	Ile	Arg	Glu	Ile	Leu	Lys	Lys	Pro					
	530					535					540									
GTT	GCT	AAG	ATG													1644				
Val	Ala	Lys	Met																	
545																				

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1664
- (D) OTHER INFORMATION: Vargula (cypridina) luciferase

(x) PUBLICATION INFORMATION:

JP 3-30678 Osaka (Tsuji)

(A) AUTHORS: Thompson et al.

(C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

(D) VOLUME: 86

(F) PAGES: 1326-1332

(G) DATE: (1989)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG	AAG	ATA	ATA	ATT	CTG	TCT	GTT	ATA	TTG	GCC	TAC	TGT	GTC	ACC	GAC	48
Met	Lys	Ile	Ile	Ile	Leu	Ser	Val	Ile	Leu	Ala	Tyr	Cys	Val	Thr	Asp	
1				5				10					15			
AAC	TGT	CAA	GAT	GCA	TGT	CCT	GTA	GAA	GCG	GAA	CCG	CCA	TCA	AGT	ACA	96
Asn	Cys	Gln	Asp	Ala	Cys	Pro	Val	Glu	Ala	Glu	Pro	Pro	Ser	Ser	Thr	

20						25				30						
CCA	ACA	GTT	CCA	ACT	TCT	TGT	GAA	GCT	AAA	GAA	GGA	GAA	TGT	ATA	GAT	144
Pro	Thr	Val	Pro	Thr	Ser	Cys	Glu	Ala	Lys	Glu	Gly	Glu	Cys	Ile	Asp	
		35					40					45				
ACC	AGA	TGC	GCA	ACA	TGT	AAA	CGA	GAT	ATA	CTA	TCA	GAT	GGA	CTG	TGT	192
Thr	Arg	Cys	Ala	Thr	Cys	Lys	Arg	Asp	Ile	Leu	Ser	Asp	Gly	Leu	Cys	
		50				55					60					
GAA	AAT	AAA	CCA	GGG	AAG	ACA	TGC	TGT	AGA	ATG	TGC	CAG	TAT	GTG	ATT	240
Glu	Asn	Lys	Pro	Gly	Lys	Thr	Cys	Cys	Arg	Met	Cys	Gln	Tyr	Val	Ile	
65					70					75				80		
GAA	TGC	AGA	GTA	GAA	GCA	GCT	GGT	TAT	TTT	AGA	ACG	TTT	TAC	GGC	AAA	288
Glu	Cys	Arg	Val	Glu	Ala	Ala	Gly	Tyr	Phe	Arg	Thr	Phe	Tyr	Gly	Lys	
				85					90					95		
AGA	TTT	AAT	TTT	CAG	GAA	CCT	GGT	AAA	TAT	GTG	CTG	GCT	AGG	GGA	ACC	336
Arg	Phe	Asn	Phe	Gln	Glu	Pro	Gly	Lys	Tyr	Val	Leu	Ala	Arg	Gly	Thr	
			100					105					110			
AAG	GGT	GGC	GAT	TGG	TCT	GTA	ACC	CTC	ACC	ATG	GAG	AAT	CTA	GAT	GGA	384
Lys	Gly	Gly	Asp	Trp	Ser	Val	Thr	Leu	Thr	Met	Glu	Asn	Leu	Asp	Gly	
		115					120					125				
CAG	AAG	GGA	GCT	GTG	CTG	ACT	AAG	ACA	ACA	CTG	GAG	GTT	GCA	GGA	GAC	432
Gln	Lys	Gly	Ala	Val	Leu	Thr	Lys	Thr	Thr	Leu	Glu	Val	Ala	Gly	Asp	
		130				135					140					
GTA	ATA	GAC	ATT	ACT	CAA	GCT	ACT	GCA	GAT	CCT	ATC	ACA	GTT	AAC	GGA	480
Val	Ile	Asp	Ile	Thr	Gln	Ala	Thr	Ala	Asp	Pro	Ile	Thr	Val	Asn	Gly	
145					150					155					160	
GGA	GCT	GAC	CCA	GTT	ATC	GCT	AAC	CCG	TTC	ACA	ATT	GGT	GAG	GTG	ACC	528
Gly	Ala	Asp	Pro	Val	Ile	Ala	Asn	Pro	Phe	Thr	Ile	Gly	Glu	Val	Thr	
				165					170					175		
ATT	GCT	GTT	GTT	GAA	ATA	CCG	GGC	TTC	AAT	ATC	ACA	GTC	ATC	GAA	TTC	576
Ile	Ala	Val	Val	Glu	Ile	Pro	Gly	Phe	Asn	Ile	Thr	Val	Ile	Glu	Phe	
			180					185					190			
TTT	AAA	CTA	ATC	GTG	ATT	GAT	ATT	CTG	GGA	GGA	AGA	TCT	GTC	AGA	ATT	624
Phe	Lys	Leu	Ile	Val	Ile	Asp	Ile	Leu	Gly	Gly	Arg	Ser	Val	Arg	Ile	
		195					200					205				
GCT	CCA	GAC	ACA	GCA	AAC	AAA	GGA	CTG	ATA	TCT	GGT	ATC	TGT	GGT	AAT	672
Ala	Pro	Asp	Thr	Ala	Asn	Lys	Gly	Leu	Ile	Ser	Gly	Ile	Cys	Gly	Asn	
		210				215					220					
CTG	GAG	ATG	AAT	GAC	GCT	GAT	GAC	TTT	ACT	ACA	GAT	GCA	GAT	CAG	CTG	720
Leu	Glu	Met	Asn	Asp	Ala	Asp	Asp	Phe	Thr	Thr	Asp	Ala	Asp	Gln	Leu	
225					230					235				240		
GCG	ATC	CAA	CCC	AAC	ATA	AAC	AAA	GAG	TTC	GAC	GGC	TGC	CCA	TTC	TAT	768
Ala	Ile	Gln	Pro	Asn	Ile	Asn	Lys	Glu	Phe	Asp	Gly	Cys	Pro	Phe	Tyr	
				245					250					255		
GGC	AAT	CCT	TCT	GAT	ATC	GAA	TAC	TGC	AAA	GGT	CTG	ATG	GAG	CCA	TAC	816
Gly	Asn	Pro	Ser	Asp	Ile	Glu	Tyr	Cys	Lys	Gly	Leu	Met	Glu	Pro	Tyr	
			260					265					270			
AGA	GCT	GTA	TGT	CGT	AAC	AAT	ATC	AAC	TTC	TAC	TAT	TAC	ACT	CTA	TCC	864
Arg	Ala	Val	Cys	Arg	Asn	Asn	Ile	Asn	Phe	Tyr	Tyr	Tyr	Thr	Leu	Ser	
		275					280						285			

TGT	GCC	TTC	GCT	TAC	TGT	ATG	GGA	GGA	GAA	GAA	AGA	GCT	AAA	CAC	GTC	912
Cys	Ala	Phe	Ala	Tyr	Cys	Met	Gly	Gly	Glu	Glu	Arg	Ala	Lys	His	Val	
	290					295					300					
CTT	TTC	GAC	TAT	GTT	GAG	ACA	TGC	GCT	GCG	CCG	GAA	ACG	AGA	GGA	ACG	960
Leu	Phe	Asp	Tyr	Val	Glu	Thr	Cys	Ala	Ala	Pro	Glu	Thr	Arg	Gly	Thr	
305					310					315					320	
TGT	GTT	TTA	TCA	GGA	CAT	ACT	TTC	TAT	GAC	ACA	TTC	GAC	AAA	GCA	AGA	1008
Cys	Val	Leu	Ser	Gly	His	Thr	Phe	Tyr	Asp	Thr	Phe	Asp	Lys	Ala	Arg	
				325					330					335		
TAT	CAA	TTC	CAG	GGC	CCA	TGC	AAG	GAG	ATT	CTG	ATG	GCC	GCA	GAC	TGT	1056
Tyr	Gln	Phe	Gln	Gly	Pro	Cys	Lys	Glu	Ile	Leu	Met	Ala	Ala	Asp	Cys	
			340					345					350			
TAC	TGG	AAC	ACA	TGG	GAT	GTA	AAG	GTT	TCA	CAT	AGA	GAC	GTC	GAA	TCA	1104
Tyr	Trp	Asn	Thr	Trp	Asp	Val	Lys	Val	Ser	His	Arg	Asp	Val	Glu	Ser	
		355					360					365				
TAC	ACT	GAG	GTA	GAG	AAA	GTA	ACA	ATC	AGG	AAA	CAG	TCA	ACT	GTA	GTA	1152
Tyr	Thr	Glu	Val	Glu	Lys	Val	Thr	Ile	Arg	Lys	Gln	Ser	Thr	Val	Val	
	370					375					380					
GAT	CTC	ATT	GTG	GAT	GGC	AAG	CAG	GTC	AAG	GTT	GGA	GGA	GTG	GAT	GTA	1200
Asp	Leu	Ile	Val	Asp	Gly	Lys	Gln	Val	Lys	Val	Gly	Gly	Val	Asp	Val	
385					390				395					400		
TCT	ATC	CCG	TAC	AGC	TCT	GAG	AAC	ACT	TCC	ATA	TAC	TGG	CAG	GAT	GGA	1248
Ser	Ile	Pro	Tyr	Ser	Ser	Glu	Asn	Thr	Ser	Ile	Tyr	Trp	Gln	Asp	Gly	
				405					410					415		
GAC	ATC	CTG	ACG	ACG	GCC	ATC	CTA	CCT	GAA	GCT	CTT	GTC	GTT	AAG	TTC	1296
Asp	Ile	Leu	Thr	Thr	Ala	Ile	Leu	Pro	Glu	Ala	Leu	Val	Val	Lys	Phe	
			420					425					430			
AAC	TTT	AAG	CAG	CTC	CTT	GTA	GTT	CAT	ATC	AGA	GAT	CCA	TTC	GAT	GCA	1344
Asn	Phe	Lys	Gln	Leu	Leu	Val	Val	His	Ile	Arg	Asp	Pro	Phe	Asp	Ala	
		435					440					445				
AAG	ACA	TGC	GGC	ATA	TGT	GGT	AAC	TAT	AAT	CAA	GAT	TCA	ACT	GAT	GAT	1392
Lys	Thr	Cys	Gly	Ile	Cys	Gly	Asn	Tyr	Asn	Gln	Asp	Ser	Thr	Asp	Asp	
	450					455					460					
TTC	TTT	GAC	GCA	GAA	GGA	GCA	TGC	GCT	CTA	ACC	CCC	AAC	CCC	CCA	GGA	1440
Phe	Phe	Asp	Ala	Glu	Gly	Ala	Cys	Ala	Leu	Thr	Pro	Asn	Pro	Pro	Gly	
465					470				475						480	
TGT	ACA	GAG	GAA	CAG	AAA	CCA	GAA	GCT	GAG	CGA	CTT	TGC	AAT	AAT	CTC	1488
Cys	Thr	Glu	Glu	Gln	Lys	Pro	Glu	Ala	Glu	Arg	Leu	Cys	Asn	Asn	Leu	
				485					490					495		
TTT	GAT	TCT	TCT	ATC	GAC	GAG	AAA	TGT	AAT	GTC	TGC	TAC	AAG	CCT	GAC	1536
Phe	Asp	Ser	Ser	Ile	Asp	Glu	Lys	Cys	Asn	Val	Cys	Tyr	Lys	Pro	Asp	
				500				505					510			
CGG	ATT	GCC	CGA	TGT	ATG	TAC	GAG	TAT	TGC	CTG	AGG	GGA	CAA	CAA	GGA	1584
Arg	Ile	Ala	Arg	Cys	Met	Tyr	Glu	Tyr	Cys	Leu	Arg	Gly	Gln	Gln	Gly	
		515					520					525				
TTT	TGT	GAC	CAT	GCT	TGG	GAG	TTC	AAG	AAA	GAA	TGC	TAC	ATA	AAA	CAT	1632
Phe	Cys	Asp	His	Ala	Trp	Glu	Phe	Lys	Lys	Glu	Cys	Tyr	Ile	Lys	His	
	530					535					540					
GGA	GAC	ACT	CTA	GAA	GTA	CCA	CCT	GAA	TGT	CAA	TAA	ACGTACAAAG				1678
Gly	Asp	Thr	Leu	Glu	Val	Pro	Pro	Glu	Cys	Gln						

545

550

555

ATACAGAAGC TAAGGCTACT ACAGCAGAAG ATAAAAAAGA AACTGTAGTT CCTTCAAAAA 1738
 CCGTGTATTT TATGTACTCA TTGTTTAATT AGAGCAAAT AAATTGTTAT TATCATAACT 1798
 TAAACTAAAA AAAAAAAAAA AA 1820

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 115...702

(D) OTHER INFORMATION: apoaeguorin-encoding gene

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,093,240

(A) AUTHORS: Inouye *et al.*

(C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

(D) VOLUME: 82

(F) PAGES: 3154-3158

(G) DATE: (1985)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG GGGAATGCAA TTCATCTTTG CATCAAAGAA      60
TTACATCAAA TCTCTAGTTG ATCAACTAAA TTGTCTCGAC AACAACAAGC AAAC ATG      117
                                     Met
                                     1

ACA AGC AAA CAA TAC TCA GTC AAG CTT ACA TCA GAC TTC GAC AAC CCA      165
Thr Ser Lys Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn Pro
                    5                      10                      15

AGA TGG ATT GGA CGA CAC AAG CAT ATG TTC AAT TTC CTT GAT GTC AAC      213
Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val Asn
                20                      25                      30

CAC AAT GGA AAA ATC TCT CTT GAC GAG ATG GTC TAC AAG GCA TCT GAT      261
His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser Asp
                35                      40                      45

ATT GTC ATC AAT AAC CTT GGA GCA ACA CCT GAG CAA GCC AAA CGA CAC      309
Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg His
                50                      55                      60

AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GGA ATG AAA TAT GGT      357
Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly
                70                      75                      80

GTG GAA ACT GAT TGG CCT GCA TAT ATT GAA GGA TGG AAA AAA TTG GCT      405
Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu Ala
                85                      90                      95

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ACT GAT GAA TTG GAG AAA TAC GCC AAA AAC GAA CCA ACG CTC ATC CGT	453
Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile Arg	
100 105 110	
ATA TGG GGT GAT GCT TTG TTT GAT ATC GTT GAC AAA GAT CAA AAT GGA	501
Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn Gly	
115 120 125	
GCC ATT ACA CTG GAT GAA TGG AAA GCA TAC ACC AAA GCT GCT GGT ATC	549
Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly Ile	
130 135 140 145	
ATC CAA TCA TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT ATT	597
Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp Ile	
150 155 160	
GAT GAA AGT GGA CAA CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT TTA	645
Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His Leu	
165 170 175	
GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT GGA	693
Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly	
180 185 190	
GCT GTC CCC TAAGAAGCTC TACGGTGGTG ATGCACCCTA GGAAGATGAT GTGATTTTGA	752
Ala Val Pro	
195	
ATAAAACACT GATGAATTCA ATCAAAATTT TCCAAATTTT TGAACGATTT CAATCGTTTG	812
TGTTGATTTT TGTAATTAGG AACAGATTAA ATCGAATGAT TAGTTGTTT TTTAATCAAC	872
AGAACTTACA AATCGAAAAA GTAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	932
AAAAAAAAAA AAAAAAAAAA AAAAAA	958

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...588
- (D) OTHER INFORMATION: Recombinant Aequorin AEQ1

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Prasher et al.
- (B) TITLE: Sequence Comparisons of Complementary DNAs Encoding Aequorin Isoforms
- (C) JOURNAL: Biochemistry
- (D) VOLUME: 26
- (F) PAGES: 1326-1332
- (G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC	48
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Met	Thr	Ser	Glu	Gln	Tyr	Ser	Val	Lys	Leu	Thr	Pro	Asp	Phe	Asp	Asn	
1				5					10					15		
CCA	AAA	TGG	ATT	GGA	CGA	CAC	AAG	CAC	ATG	TTT	AAT	TTT	CTT	GAT	GTC	96
Pro	Lys	Trp	Ile	Gly	Arg	His	Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	
			20					25					30			
AAC	CAC	AAT	GGA	AGG	ATC	TCT	CTT	GAC	GAG	ATG	GTC	TAC	AAG	GCG	TCC	144
Asn	His	Asn	Gly	Arg	Ile	Ser	Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser	
		35					40					45				
GAT	ATT	GTT	ATA	AAC	AAT	CTT	GGA	GCA	ACA	CCT	GAA	CAA	GCC	AAA	CGT	192
Asp	Ile	Val	Ile	Asn	Asn	Leu	Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg	
	50					55					60					
CAC	AAA	GAT	GCT	GTA	GAA	GCC	TTC	TTC	GGA	GGA	GCT	GGA	ATG	AAA	TAT	240
His	Lys	Asp	Ala	Val	Glu	Ala	Phe	Phe	Gly	Gly	Ala	Gly	Met	Lys	Tyr	
65					70				75						80	
GGT	GTA	GAA	ACT	GAA	TGG	CCT	GAA	TAC	ATC	GAA	GGA	TGG	AAA	AGA	CTG	288
Gly	Val	Glu	Thr	Glu	Trp	Pro	Glu	Tyr	Ile	Glu	Gly	Trp	Lys	Arg	Leu	
				85					90					95		
GCT	TCC	GAG	GAA	TTG	AAA	AGG	TAT	TCA	AAA	AAC	CAA	ATC	ACA	CTT	ATT	336
Ala	Ser	Glu	Glu	Leu	Lys	Arg	Tyr	Ser	Lys	Asn	Gln	Ile	Thr	Leu	Ile	
			100					105					110			
CGT	TTA	TGG	GGT	GAT	GCA	TTG	TTC	GAT	ATC	ATT	GAC	AAA	GAC	CAA	AAT	384
Arg	Leu	Trp	Gly	Asp	Ala	Leu	Phe	Asp	Ile	Ile	Asp	Lys	Asp	Gln	Asn	
		115					120					125				
GGA	GCT	ATT	TCA	CTG	GAT	GAA	TGG	AAA	GCA	TAC	ACC	AAA	TCT	GAT	GGC	432
Gly	Ala	Ile	Ser	Leu	Asp	Glu	Trp	Lys	Ala	Tyr	Thr	Lys	Ser	Asp	Gly	
	130					135					140					
ATC	ATC	CAA	TCG	TCA	GAA	GAT	TGC	GAG	GAA	ACA	TTC	AGA	GTG	TGC	GAT	480
Ile	Ile	Gln	Ser	Ser	Glu	Asp	Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp	
145					150				155						160	
ATT	GAT	GAA	AGT	GGA	CAG	CTC	GAT	GTT	GAT	GAG	ATG	ACA	AGA	CAA	CAT	528
Ile	Asp	Glu	Ser	Gly	Gln	Leu	Asp	Val	Asp	Glu	Met	Thr	Arg	Gln	His	
				165				170						175		
TTA	GGA	TTT	TGG	TAC	ACC	ATG	GAT	CCT	GCT	TGC	GAA	AAG	CTC	TAC	GGT	576
Leu	Gly	Phe	Trp	Tyr	Thr	Met	Asp	Pro	Ala	Cys	Glu	Lys	Leu	Tyr	Gly	
			180					185					190			
GGA	GCT	GTC	CCC	TAA												591
Gly	Ala	Val	Pro	*												
			195													

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...588
 (D) OTHER INFORMATION: Recombinant Aequorin AEQ2

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Prasher et al.
 (B) TITLE: Sequence Comparisons of Complementary
 DNAs Encoding Aequorin Isotypes
 (C) JOURNAL: Biochemistry
 (D) VOLUME: 26
 (F) PAGES: 1326-1332
 (G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA TCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn	
1 5 10 15	
CCA AGA TGG ATT GGA CGA CAC AAG CAT ATG TTC AAT TTC CTT GAT GTC	96
Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
AAC CAC AAT GGA AAA ATC TCT CTT GAC GAG ATG GTC TAC AAG GCA TCT	144
Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
GAT ATT GTC ATC AAT AAC CTT GGA GCA ACA CCT GAG CAA GCC AAA CGA	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GGA ATG AAA TAT	240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr	
65 70 75 80	
GGT GTG GAA ACT GAT TGG CCT GCA TAT ATT GAA GGA TGG AAA AAA TTG	288
Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu	
85 90 95	
GCT ACT GAT GAA TTG GAG AAA TAC GCC AAA AAC GAA CCA ACG CTC ATC	336
Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile	
100 105 110	
CGT ATA TGG GGT GAT GCT TTG TTC GAT ATC GTT GAC AAA GAT CAA AAT	384
Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn	
115 120 125	
GGA GCC ATT ACA CTG GAT GAA TGG AAA GCA TAC ACC AAA GCT GCT GGT	432
Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly	
130 135 140	
ATC ATC CAA TCA TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT	480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp	
145 150 155 160	
ATT GAT GAA AGT GGA CAA CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT	528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His	
165 170 175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT	576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly	
180 185 190	

GGA GCT GTC CCC TAA
 Gly Ala Val Pro *
 195

591

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...588

(D) OTHER INFORMATION: Recombinant Aequorin AEQ3

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Prasher et al.

(B) TITLE: Sequence Comparisons of Complementary
DNAs Encoding Aequorin Isotypes

(C) JOURNAL: Biochemistry

(D) VOLUME: 26

(F) PAGES: 1326-1332

(G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA TCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn	
1 5 10 15	
CCA AGA TGG ATT GGA CGA CAC AAG CAT ATG TTC AAT TTC CTT GAT GTC	96
Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
AAC CAC AAT GGA AAA ATC TCT CTT GAC GAG ATG GTC TAC AAG GCA TCT	144
Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
GAT ATT GTC ATC AAT AAC CTT GGA GCA ACA CCT GAG CAA GCC AAA CGA	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
CAC AAA GAT GCT GTA GGA GAC TTC TTC GGA GGA GCT GGA ATG AAA TAT	240
His Lys Asp Ala Val Gly Asp Phe Phe Gly Gly Ala Gly Met Lys Tyr	
65 70 75 80	
GGT GTG GAA ACT GAT TGG CCT GCA TAC ATT GAA GGA TGG AAA AAA TTG	288
Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu	
85 90 95	
GCT ACT GAT GAA TTG GAG AAA TAC GCC AAA AAC GAA CCA ACG CTC ATC	336
Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile	
100 105 110	
CGT ATA TGG GGT GAT GCT TTG TTC GAT ATC GTT GAC AAA GAT CAA AAT	384
Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn	

115	120	125	
GGA GCC ATT ACA CTG GAT GAA TGG AAA GCA TAC ACC AAA GCT GCT GGT			432
Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly			
130	135	140	
ATC ATC CAA TCA TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT			480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp			
145	150	155	160
ATT GAT GAA AAT GGA CAA CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT			528
Ile Asp Glu Asn Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His			
	165	170	175
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT			576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly			
	180	185	190
GGA GCT GTC CCC TAA			591
Gly Ala Val Pro *			
195			

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...567
- (D) OTHER INFORMATION: Aequorin photoprotein

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Charbonneau et al.
- (B) TITLE: Amino acid sequence of the calcium-dependent photoprotein aequorin
- (C) JOURNAL: Am. Chem. Soc.
- (D) VOLUME: 24
- (E) ISSUE: 24
- (F) PAGES: 6762-6771
- (G) DATE: 1985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTC AAG CTT ACA CCA GAC TTC GAC AAC CCA AAA TGG ATT GGA CGA CAC	48
Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His	
1	5
AAG CAC ATG TTT AAT TTT CTT GAT GTC AAC CAC AAT GGA AGG ATC TCT	96
Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser	
20	25
CTT GAC GAG ATG GTC TAC AAG GCG TCC GAT ATT GTT ATA AAC AAT CTT	144
Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu	

35	40	45	
GGA GCA ACA CCT GAA CAA GCC AAA CGT CAC AAA GAT GCT GTA GAA GCC			192
Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala			
50	55	60	
TTC TTC GGA GGA GCT GCA ATG AAA TAT GGT GTA GAA ACT GAA TGG CCT			240
Phe Phe Gly Gly Ala Ala Met Lys Tyr Gly Val Glu Thr Glu Trp Pro			
65	70	75	80
GAA TAC ATC GAA GGA TGG AAA AGA CTG GCT TCC GAG GAA TTG AAA AGG			288
Glu Tyr Ile Glu Gly Trp Lys Arg Leu Ala Ser Glu Glu Leu Lys Arg			
85	90	95	
TAT TCA AAA AAC CAA ATC ACA CTT ATT CGT TTA TGG GGT GAT GCA TTG			336
Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu			
100	105	110	
TTC GAT ATC ATT GAC AAA GAC CAA AAT GGA GCT ATT TCA CTG GAT GAA			384
Phe Asp Ile Ile Asp Lys Asp Gln Asn Gly Ala Ile Ser Leu Asp Glu			
115	120	125	
TGG AAA GCA TAC ACC AAA TCT GCT GGC ATC ATC CAA TCG TCA GAA GAT			432
Trp Lys Ala Tyr Thr Lys Ser Ala Gly Ile Ile Gln Ser Ser Glu Asp			
130	135	140	
TGC GAG GAA ACA TTC AGA GTG TGC GAT ATT GAT GAA AGT GGA CAG CTC			480
Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu			
145	150	155	160
GAT GTT GAT GAG ATG ACA AGA CAA CAT TTA GGA TTT TGG TAC ACC ATG			528
Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met			
165	170	175	
GAT CCT GCT TGC GAA AAG CTC TAC GGT GGA GCT GTC CCC			567
Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro			
180	185		

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...588

(D) OTHER INFORMATION: Aequorin mutant w/increased bioluminescence activity

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(K) RELEVANT RESIDUES IN SEQ ID NO: 10:

Asp 124 changed to Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn	
1 5 10 15	
CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC	96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC	144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GCA ATG AAA TAT	240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr	
65 70 75 80	
GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG	288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu	
85 90 95	
GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT	336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile	
100 105 110	
CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT TCC AAA GAC CAA AAT	384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn	
115 120 125	
GGA GCT ATT TCA CTG GAT GAA TGG AAA GCA TAC ACC AAA TCT GCT GGC	432
Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly	
130 135 140	
ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT	480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp	
145 150 155 160	
ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT	528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His	
165 170 175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT	576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly	
180 185 190	
GGA GCT GTC CCC	588
Gly Ala Val Pro	
195	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...588
 (D) OTHER INFORMATION: Recombinant site-directed Aequorin mutant
 w/increased biolum. activity

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(K) RELEVANT RESIDUES IN SEQ ID NO: 11:
 Glu 135 changed to Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG	ACC	AGC	GAA	CAA	TAC	TCA	GTC	AAG	CTT	ACA	CCA	GAC	TTC	GAC	AAC	48
Met	Thr	Ser	Glu	Gln	Tyr	Ser	Val	Lys	Leu	Thr	Pro	Asp	Phe	Asp	Asn	
1				5					10					15		
CCA	AAA	TGG	ATT	GGA	CGA	CAC	AAG	CAC	ATG	TTT	AAT	TTT	CTT	GAT	GTC	96
Pro	Lys	Trp	Ile	Gly	Arg	His	Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	
			20					25					30			
AAC	CAC	AAT	GGA	AGG	ATC	TCT	CTT	GAC	GAG	ATG	GTC	TAC	AAG	GCG	TCC	144
Asn	His	Asn	Gly	Arg	Ile	Ser	Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser	
			35					40				45				
GAT	ATT	GTT	ATA	AAC	AAT	CTT	GGA	GCA	ACA	CCT	GAA	CAA	GCC	AAA	CGT	192
Asp	Ile	Val	Ile	Asn	Asn	Leu	Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg	
	50					55					60					
CAC	AAA	GAT	GCT	GTA	GAA	GCC	TTC	TTC	GGA	GGA	GCT	GCA	ATG	AAA	TAT	240
His	Lys	Asp	Ala	Val	Glu	Ala	Phe	Phe	Gly	Gly	Ala	Ala	Met	Lys	Tyr	
65					70				75						80	
GGT	GTA	GAA	ACT	GAA	TGG	CCT	GAA	TAC	ATC	GAA	GGA	TGG	AAA	AGA	CTG	288
Gly	Val	Glu	Thr	Glu	Trp	Pro	Glu	Tyr	Ile	Glu	Gly	Trp	Lys	Arg	Leu	
				85					90					95		
GCT	TCC	GAG	GAA	TTG	AAA	AGG	TAT	TCA	AAA	AAC	CAA	ATC	ACA	CTT	ATT	336
Ala	Ser	Glu	Glu	Leu	Lys	Arg	Tyr	Ser	Lys	Asn	Gln	Ile	Thr	Leu	Ile	
			100					105					110			
CGT	TTA	TGG	GGT	GAT	GCA	TTG	TTC	GAT	ATC	ATT	TCC	AAA	GAC	CAA	AAT	384
Arg	Leu	Trp	Gly	Asp	Ala	Leu	Phe	Asp	Ile	Ile	Ser	Lys	Asp	Gln	Asn	
		115					120					125				
GGA	GCT	ATT	TCA	CTG	GAT	TCA	TGG	AAA	GCA	TAC	ACC	AAA	TCT	GCT	GGC	432
Gly	Ala	Ile	Ser	Leu	Asp	Ser	Trp	Lys	Ala	Tyr	Thr	Lys	Ser	Ala	Gly	
	130					135					140					
ATC	ATC	CAA	TCG	TCA	GAA	GAT	TGC	GAG	GAA	ACA	TTC	AGA	GTG	TGC	GAT	480
Ile	Ile	Gln	Ser	Ser	Glu	Asp	Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp	
145					150				155						160	
ATT	GAT	GAA	AGT	GGA	CAG	CTC	GAT	GTT	GAT	GAG	ATG	ACA	AGA	CAA	CAT	528
Ile	Asp	Glu	Ser	Gly	Gln	Leu	Asp	Val	Asp	Glu	Met	Thr	Arg	Gln	His	
				165				170						175		
TTA	GGA	TTT	TGG	TAC	ACC	ATG	GAT	CCT	GCT	TGC	GAA	AAG	CTC	TAC	GGT	576
Leu	Gly	Phe	Trp	Tyr	Thr	Met	Asp	Pro	Ala	Cys	Glu	Lys	Leu	Tyr	Gly	

180

185

190

GGA GCT GTC CCC
Gly Ala Val Pro
195

588

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...588

(D) OTHER INFORMATION: Recombinant site-directed
Aequorin mutant w/increased biolum. activity

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn	
1 5 10 15	
CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC	96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC	144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GCA ATG AAA TAT	240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr	
65 70 75 80	
GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG	288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu	
85 90 95	
GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT	336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile	
100 105 110	
CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT TCC AAA GAC CAA AAT	384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn	
115 120 125	
GCA GCT ATT TCA CTG GAT GAA TGG AAA GCA TAC ACC AAA TCT GCT GGC	432
Ala Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly	

130	135	140	
ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT			480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp			
145	150	155	160
ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT			528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His			
	165	170	175
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT			576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly			
	180	185	190
GGA GCT GTC CCC			588
Gly Ala Val Pro			
	195		

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...567
- (D) OTHER INFORMATION: Recombinant apoaeguorin (AQUALITE®)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTC AAG CTT ACA CCA GAC TTC GAC AAC CCA AAA TGG ATT GGA CGA CAC	48
Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His	
1	5
AAG CAC ATG TTT AAT TTT CTT GAT GTC AAC CAC AAT GGA AGG ATC TCT	96
Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser	
	20
CTT GAC GAG ATG GTC TAC AAG GCG TCC GAT ATT GTT ATA AAC AAT CTT	144
Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu	
	35
GGA GCA ACA CCT GAA CAA GCC AAA CGT CAC AAA GAT GCT GTA GAA GCC	192
Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala	
	50
TTC TTC GGA GGA GCT GGA ATG AAA TAT GGT GTA GAA ACT GAA TGG CCT	240
Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Glu Trp Pro	
	65
GAA TAC ATC GAA GGA TGG AAA AAA CTG GCT TCC GAG GAA TTG AAA AGG	288
Glu Tyr Ile Glu Gly Trp Lys Lys Leu Ala Ser Glu Glu Leu Lys Arg	
	85
TAT TCA AAA AAC CAA ATC ACA CTT ATT CGT TTA TGG GGT GAT GCA TTG	336
Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu	
	100
TTC GAT ATC ATT GAC AAA GAC CAA AAT GGA GCT ATT CTG TCA GAT GAA	384

Phe	Asp	Ile	Ile	Asp	Lys	Asp	Gln	Asn	Gly	Ala	Ile	Leu	Ser	Asp	Glu		
		115					120					125					
TGG	AAA	GCA	TAC	ACC	AAA	TCT	GAT	GGC	ATC	ATC	CAA	TCG	TCA	GAA	GAT	432	
Trp	Lys	Ala	Tyr	Thr	Lys	Ser	Asp	Gly	Ile	Ile	Gln	Ser	Ser	Glu	Asp		
		130					135				140						
TGC	GAG	GAA	ACA	TTC	AGA	GTG	TGC	GAT	ATT	GAT	GAA	AGT	GGA	CAG	CTC	480	
Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp	Ile	Asp	Glu	Ser	Gly	Gln	Leu		
		145				150				155					160		
GAT	GTT	GAT	GAG	ATG	ACA	AGA	CAA	CAT	TTA	GGA	TTT	TGG	TAC	ACC	ATG	528	
Asp	Val	Asp	Glu	Met	Thr	Arg	Gln	His	Leu	Gly	Phe	Trp	Tyr	Thr	Met		
				165					170						175		
GAT	CCT	GCT	TGC	GAA	AAG	CTC	TAC	GGT	GGA	GCT	GTC	CCC				567	
Asp	Pro	Ala	Cys	Glu	Lys	Leu	Tyr	Gly	Ala	Val	Pro						
			180					185									

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,484,723

(ix) FEATURE:

(D) OTHER INFORMATION: *Vibrio fisheri* Flavin reductase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Pro	Ile	Asn	Cys	Lys	Val	Lys	Ser	Ile	Glu	Pro	Leu	Ala	Cys	Asn		
1				5					10					15			
Thr	Phe	Arg	Ile	Leu	Leu	His	Pro	Glu	Gln	Pro	Val	Ala	Phe	Lys	Ala		
			20					25					30				
Gly	Gln	Tyr	Leu	Thr	Val	Val	Met	Gly	Glu	Lys	Asp	Lys	Arg	Pro	Phe		
		35					40				45						
Ser	Ile	Ala	Ser	Ser	Pro	Cys	Arg	His	Glu	Gly	Glu	Ile	Glu	Leu	His		
		50				55					60						
Ile	Gly	Ala	Ala	Glu	His	Asn	Ala	Tyr	Ala	Gly	Glu	Val	Val	Glu	Ser		
	65				70				75					80			
Met	Lys	Ser	Ala	Leu	Glu	Thr	Gly	Gly	Asp	Ile	Leu	Ile	Asp	Ala	Pro		
			85					90						95			
His	Gly	Glu	Ala	Trp	Ile	Arg	Glu	Asp	Ser	Asp	Arg	Ser	Met	Leu	Leu		
			100					105					110				
Ile	Ala	Gly	Gly	Thr	Gly	Phe	Ser	Tyr	Val	Arg	Ser	Ile	Leu	Asp	His		
		115					120					125					
Cys	Ile	Ser	Gln	Gln	Ile	Gln	Lys	Pro	Ile	Tyr	Leu	Tyr	Trp	Gly	Gly		
		130				135					140						
Arg	Asp	Glu	Cys	Gln	Leu	Tyr	Ala	Lys	Ala	Glu	Leu	Glu	Ser	Ile	Ala		

145		150		155		160									
Gln	Ala	His	Ser	His	Ile	Thr	Phe	Val	Pro	Val	Val	Glu	Lys	Ser	Glu
				165					170					175	
Gly	Trp	Thr	Gly	Lys	Thr	Gly	Asn	Val	Leu	Glu	Ala	Val	Lys	Ala	Asp
			180					185					190		
Phe	Asn	Ser	Leu	Ala	Asp	Met	Asp	Ile	Tyr	Ile	Ala	Gly	Arg	Phe	Glu
		195					200					205			
Met	Ala	Gly	Ala	Ala	Arg	Glu	Gln	Phe	Thr	Thr	Glu	Lys	Gln	Ala	Lys
	210					215					220				
Lys	Glu	Gln	Leu	Phe	Gly	Asp	Ala	Phe	Ala	Phe	Ile				
225					230					235					